SEQUENCE LISTING

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<120> NOVEL MOUSE CXC CHEMOKINE RECEPTOR

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<170> PatentIn Ver. 2.0

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atg gaa ccg atc agt gtg agt ata tac act tct gat aac tac tct gaa 167
Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu
1 5 10 15

gaa gtg ggg tct gga gac tat gac tcc aac aag gaa ccc tgc ttc cgg 215
Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
20 25 30

gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc atc tac ttc 263
Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
35 40 45

atc atc ttc ttg act ggc ata gtc ggc aat gga ttg gtg atc ctg gtc 311

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Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
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atg ggt tac cag aag aag cta agg agc atg acg gac aag tac cgg ctg   359
Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
 65                  70                  75                  80

cac ctg tca gtg gct gac ctc ctc ttt gtc atc aca ctc ccc ttc tgg   407
His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
                85                  90                  95

gca gtt gat gcc atg gct gac tgg tac ttt ggg aaa ttt ttg tgt aag   455
Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
            100                 105                 110

gct gtc cat atc atc tac act gtc aac ctc tac agc agc gtt ctc atc   503
Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
        115                 120                 125

ctg gcc ttc atc agc ctg gac cgg tac ctc gcc att gtc cac gcc acc   551
Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
    130                 135                 140

aac agt caa agg cca agg aaa ctg ctg gct gaa aag gca gtc tat gtg   599
Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
145                 150                 155                 160

ggc gtc tgg atc cca gcc ctc ctc ctg act ata cct gac ttc atc ttt   647
Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
                165                 170                 175

gcc gac gtc agc cag ggg gac atc agt cag ggg gat gac agg tac atc   695
Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
            180                 185                 190

tgt gac cgc ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc   743
Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
        195                 200                 205

cag cat ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc   791
Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser
    210                 215                 220

tgt tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac cag   839
Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
225                 230                 235                 240

aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc ttt   887
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Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
                245                 250                 255

gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc ttc atc   935
Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
            260                 265                 270

ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc att gtg cac   983
Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
        275                 280                 285

aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc cac tgt tgc ctg   1031
Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu
    290                 295                 300

aac ccc atc ctc tat gcc ttc ctc ggg gcc aag ttc aaa agc tct gcc   1079
Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
305                 310                 315                 320

cag cat gca ctc aac tcc atg agc aga ggc tcc agc ctc aag atc ctt   1127
Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
                325                 330                 335

tcc aaa gga aag cgg ggt gga cac tct tcc gtc tcc acg gag tca gaa   1175
Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
            340                 345                 350

tcc tcc agt ttt cac tcc agc taacccttat gcaaagactt atataatata      1226
Ser Ser Ser Phe His Ser Ser
        355

tatatatata tgataaagaa ctttttttatg ttacacattt tccagatata agagactgac 1286

cagtcttgta cagtttttt ttttttttaa ttgactgttg ggagtttatg ttcctctagt 1346

ttttgtgagg tttgacttaa tttatataaa tattgttttt tgtttgtttc atgtgaatga 1406

gcgtctaggc aggacctgtg gccaagttct tagtagctgt ttatctgtgt gtaggactgt 1466

agaactgtag aggaagaaac tgaacattcc agaatgtgtg gtaaattgaa taaagctagc 1526

cgtgatcctc agctgttgct gcataatctc ttcattccga ggagcacccc acccccaccc 1586

ccacccccac cccattctta aattgtttgg ttatgctgtg tgatggtttg tttggttttt 1646

ttttgttgtt gttgttgttt tttttttctg taaaagatgg cacttaaaac caaagcctga 1706

aatggtggta gaaatgctgg ggtttttttt gtttgtttgt tttttcagtt ttcaagagta 1766
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gattgacttc agtccctaca aatgtacagt cttgtattac attgttaata aaagtcaatg 1826

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<213> Mus sp.

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             20                  25                  30

Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
         35                  40                  45

Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
     50                  55                  60

Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
 65                  70                  75                  80

His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
                 85                  90                  95

Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
            100                 105                 110

Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
        115                 120                 125

Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
    130                 135                 140

Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
145                 150                 155                 160

Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
                165                 170                 175

Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
            180                 185                 190
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Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
        195                 200                 205

Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser
    210                 215                 220

Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
225                 230                 235                 240

Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
                245                 250                 255

Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
            260                 265                 270

Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
        275                 280                 285

Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu
    290                 295                 300

Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
305                 310                 315                 320

Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
                325                 330                 335

Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
            340                 345                 350

Ser Ser Ser Phe His Ser Ser
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Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe
  1               5                  10                  15
```

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tgg gca gtt gat gcc atg gct gac tgg tac ttt ggg aaa ttt ttg tgt   96
Trp Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys
             20                  25                  30

aag gct gtc cat atc atc tac act gtc aac ctc tac agc agc gtt ctc   144
Lys Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu
         35                  40                  45

atc ctg gcc ttc atc agc ctg gac cgg tac ctc gcc att gtc cac gcc   192
Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala
     50                  55                  60

acc aac agt caa agg cca agg aaa ctg ctg gct gaa aag gca gtc tat   240
Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr
 65                  70                  75                  80

gtg ggc gtc tgg atc cca gcc ctc ctc ctg act ata cct gac ttc atc   288
Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile
                 85                  90                  95

ttt gcc gac gtc agc cag ggg gac atc agt cag ggg gat gac agg tac   336
Phe Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr
            100                 105                 110

atc tgt gac cgc ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa   384
Ile Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln
        115                 120                 125

ttc cag cat ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc   432
Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu
    130                 135                 140

tcc tgt tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac   480
Ser Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His
145                 150                 155                 160

cag aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc   528
Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
                165                 170                 175

ttt gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc ttc   576
Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe
            180                 185                 190

atc ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc att gtg   624
Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val
        195                 200                 205
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cac aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc cac tgt tgc   672
His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys
    210                 215                 220

ctg aac ccc atc ctc tat                                         690
Leu Asn Pro Ile Leu Tyr
225                 230
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  1               5                  10                  15

Trp Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys
             20                  25                  30

Lys Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu
         35                  40                  45

Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala
     50                  55                  60

Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr
 65                  70                  75                  80

Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile
                 85                  90                  95

Phe Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr
            100                 105                 110

Ile Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln
        115                 120                 125

Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu
    130                 135                 140

Ser Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His
145                 150                 155                 160

Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
                165                 170                 175
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Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe
            180                 185                 190

Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val
        195                 200                 205

His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys
    210                 215                 220

Leu Asn Pro Ile Leu Tyr
225                 230
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<210> 5
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<212> DNA
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tgaccctctg aggcgtttgg tgctccggta accaccacgg ctgtagagcg agtgttgcc  119

atg gaa ccg atc agt gtg agt ata tac act tct gat aac tac tct gaa   167
Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu
  1               5                  10                  15

gaa gtg ggg tct gga gac tat gac tcc aac aag gaa ccc tgc ttc cgg   215
Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
             20                  25                  30

gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc atc tac ttc   263
Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
         35                  40                  45

atc atc ttc ttg act ggc ata gtc ggc aat gga ttg gtg atc ctg gtc   311
Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
     50                  55                  60

atg ggt tac cag aag aag cta agg agc atg acg gac aag tac cgg ctg   359
Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
 65                  70                  75                  80

cac ctg tca gtg gct gac ctc ctc ttt gtc atc aca ctc ccc ttc tgg   407
```

```
His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
                 85                  90                  95

gca gtt gat gcc atg gct gac tgg tac ttt ggg aaa ttt ttg tgt aag   455
Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
            100                 105                 110

gct gtc cat atc atc tac act gtc aac ctc tac agc agc gtt ctc atc   503
Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
        115                 120                 125

ctg gcc ttc atc agc ctg gac cgg tac ctc gcc att gtc cac gcc acc   551
Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
    130                 135                 140

aac agt caa agg cca agg aaa ctg ctg gct gaa aag gca gtc tat gtg   599
Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
145                 150                 155                 160

ggc gtc tgg atc cca gcc ctc ctc ctg act ata cct gac ttc atc ttt   647
Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
                165                 170                 175

gcc gac gtc agc cag ggg gac atc agt cag ggg gat ga               685
Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp
            180                 185
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Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
             20                  25                  30

Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
         35                  40                  45

Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
     50                  55                  60

Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
 65                  70                  75                  80
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His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
                 85                  90                  95

Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
            100                 105                 110

Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
        115                 120                 125

Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
    130                 135                 140

Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
145                 150                 155                 160

Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
                165                 170                 175

Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp
            180                 185


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<212> DNA
<213> Mus sp.

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<221> CDS
<222> (1)..(1056)

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Ile Tyr Thr Ser Asp Asn Tyr Ser Glu Glu Val Gly Ser Gly Asp Tyr
  1               5                  10                  15

gac tcc aac aag gaa ccc tgc ttc cgg gat gaa aac gtc cat ttc aat   96
Asp Ser Asn Lys Glu Pro Cys Phe Arg Asp Glu Asn Val His Phe Asn
             20                  25                  30

agg atc ttc ctg ccc acc atc tac ttc atc atc ttc ttg act ggc ata   144
Arg Ile Phe Leu Pro Thr Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile
         35                  40                  45

gtc ggc aat gga ttg gtg atc ctg gtc atg ggt tac cag aag aag cta   192
Val Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu
     50                  55                  60
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```
agg agc atg acg gac aag tac cgg ctg cac ctg tca gtg gct gac ctc   240
Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu
 65                  70                  75                  80

ctc ttt gtc atc aca ctc ccc ttc tgg gca gtt gat gcc atg gct gac   288
Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp
                85                  90                  95

tgg tac ttt ggg aaa ttt ttg tgt aag gct gtc cat atc atc tac act   336
Trp Tyr Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr
            100                 105                 110

gtc aac ctc tac agc agc gtt ctc atc ctg gcc ttc atc agc ctg gac   384
Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
        115                 120                 125

cgg tac ctc gcc att gtc cac gcc acc aac agt caa agg cca agg aaa   432
Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys
    130                 135                 140

ctg ctg gct gaa aag gca gtc tat gtg ggc gtc tgg atc cca gcc ctc   480
Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro Ala Leu
145                 150                 155                 160

ctc ctg act ata cct gac ttc atc ttt gcc gac gtc agc cag ggg gac   528
Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser Gln Gly Asp
                165                 170                 175

atc agt cag ggg gat gac agg tac atc tgt gac cgc ctt tac ccc gat   576
Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg Leu Tyr Pro Asp
            180                 185                 190

agc ctg tgg atg gtg gtg ttt caa ttc cag cat ata atg gtg ggt ctc   624
Ser Leu Trp Met Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
        195                 200                 205

atc ctg ccc ggc atc gtc atc ctc tcc tgt tac tgc atc atc atc tct   672
Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser
    210                 215                 220

aag ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acg   720
Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
225                 230                 235                 240

aca gtc atc ctc atc cta gct ttc ttt gcc tgc tgg ctg cca tat tat   768
Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
                245                 250                 255
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gtg ggg atc agc atc gac tcc ttc atc ctt ttg gga gtc atc aag caa   816
Val Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Gly Val Ile Lys Gln
            260                 265                 270

gga tgt gac ttc gag agc att gtg cac aag tgg atc tcc atc aca gag   864
Gly Cys Asp Phe Glu Ser Ile Val His Lys Trp Ile Ser Ile Thr Glu
        275                 280                 285

gcc ctc gcc ttc ttc cac tgt tgc ctg aac ccc atc ctc tat gcc ttc   912
Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
    290                 295                 300

ctc ggg gcc aag ttc aaa agc tct gcc cag cat gca ctc aac tcc atg   960
Leu Gly Ala Lys Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met
305                 310                 315                 320

agc aga ggc tcc agc ctc aag atc ctt tcc aaa gga aag cgg ggt gga   1008
Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
                325                 330                 335

cac tct tcc gtc tcc acg gag tca gaa tcc tcc agt ttt cac tcc agc   1056
His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
            340                 345                 350

taacccttat gcaaagactt atataatata tatatatata tgataaagaa ctttttttatg 1116

ttacacattt tccagatata agagactgac cagtcttgta cagtttttt ttttttttaa 1176

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ttcattccga ggagcacccc acccccaccc ccacccccac cccattctta aattgtttgg 1476

ttatgctgtg tgatggtttg tttggttttt ttttgttgtt gttgttgttt ttttttttctg 1536

taaaagatgg cacttaaaac caaagcctga atggtggta gaaatgctgg ggtttttttt 1596

gtttgtttgt tttttcagtt ttcaagagta gattgacttc agtccctaca aatgtacagt 1656

cttgtattac attgttaata aaagtcaatg ataaactt                        1694
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<213> Mus sp.

<400> 8

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Asp Ser Asn Lys Glu Pro Cys Phe Arg Asp Glu Asn Val His Phe Asn
             20                  25                  30

Arg Ile Phe Leu Pro Thr Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile
         35                  40                  45

Val Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu
     50                  55                  60

Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu
 65                  70                  75                  80

Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp
                 85                  90                  95

Trp Tyr Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr
            100                 105                 110

Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
        115                 120                 125

Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys
    130                 135                 140

Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro Ala Leu
145                 150                 155                 160

Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser Gln Gly Asp
                165                 170                 175

Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg Leu Tyr Pro Asp
            180                 185                 190

Ser Leu Trp Met Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
        195                 200                 205

Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser
    210                 215                 220
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Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
225                 230                 235                 240

Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
                245                 250                 255

Val Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Gly Val Ile Lys Gln
            260                 265                 270

Gly Cys Asp Phe Glu Ser Ile Val His Lys Trp Ile Ser Ile Thr Glu
        275                 280                 285

Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
    290                 295                 300

Leu Gly Ala Lys Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met
305                 310                 315                 320

Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
                325                 330                 335

His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
            340                 345                 350
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<210> 9
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<222> (13)
<223> i

<220>
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<223> i

<400> 9
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<210> 10

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<220>
<221> modified_base
<222> (8)..(9)
<223> i

<220>
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<223> i

<400> 10
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<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 11
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<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 12
ccatcctaat acgactcact atagggc 27

<210> 13
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 15
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<210> 16
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 16
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<210> 17
<211> 27
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 17
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<210> 18
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<220>
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<400> 18
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<210> 19
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<212> DNA
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<220>
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<400> 19
ctgcacctgt cagtggctga 20

<210> 20
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 20
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<210> 21
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<213> Mus musculus

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<222> (59)..(325)

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Met Asp Ala Lys Val Val Ala Val Leu Ala Leu Val Leu Ala Ala Leu
 1 5 10 15

tgc atc agt gac ggt aaa cca gtc agc ctg agc tac cga tgc ccc tgc 154
Cys Ile Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
 20 25 30

cgg ttc ttc gag agc cac atc gcc aga gcc aac gtc aag cat ctg aaa 202
Arg Phe Phe Glu Ser His Ile Ala Arg Ala Asn Val Lys His Leu Lys
 35 40 45

atc ctc aac act cca aac tgt gcc ctt cag att gtt gca cgg ctg aag 250
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
 50 55 60

aac aac aac aga caa gtg tgc att gac ccg aaa tta aag tgg atc caa 298
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
 65 70 75 80

gag tac ctg gag aaa gct tta aac aag taagcacaac agcccaaagg 345
Glu Tyr Leu Glu Lys Ala Leu Asn Lys
 85

actttccagt agacccccga ggaaggctga catccgtggg agatgcaagg gcagtggtgg 405

ggaggagggc ctgaaccctg gccaggatgg ccggcgggac agcactgact ggggtcatgc 465

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ttcatccctg ccctcgcccg tgcacaatgg agcttttata actggggttt ttctaaggaa 585

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aaagcagtga ttacttcaag ggctgtattc agtttgcttt ggagcttctc tttgccctgg 705

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gtcaattcat atatttgaag tggagccata gtaatgccag tagatatctc tatgatcttg 1605

agctactggc aacttgtaaa gaaatatata tgacatataa atgtattgta gctttccggt 1665

gtcagccacg gtgtatttttt ccacttggaa tgaaattgta tcaactgtga cattatatgc 1725

actagcaata aaatgctaat tgtttcatgc tgtaaaaaaa aaaaaaaaaa a 1776

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<212> PRT
<213> Mus musculus

<400> 22
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Cys Ile Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
20 25 30

Arg Phe Phe Glu Ser His Ile Ala Arg Ala Asn Val Lys His Leu Lys
35 40 45

Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
50 55 60

Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65 70 75 80

Glu Tyr Leu Glu Lys Ala Leu Asn Lys
85